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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:48:26 ; Search time 100 Seconds  
(without alignments)  
210.958 Million cell updates/sec

Title: pct-US03-05305-4

Perfect score: 21

Sequence: 1 cagcagcaggatcttcataat 21

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched: 639749 seqs, 50280978 residues

Total number of hits satisfying chosen parameters: 370718

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/2/pubpna/PCN2\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/2/pubpna/PCNUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/2/pubpna/US10\_PUB.seq:\*

12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*

13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match | Length | DB                 | ID | Description         |
|------------|-------|-------|-------|--------|--------------------|----|---------------------|
| 1          | 21    | 100.0 | 21    | 10     | US-09-944-326-4    |    | Sequence 4, Appli   |
| 2          | 14.8  | 70.5  | 21    | 10     | US-09-944-326-1    |    | Sequence 1, Appli   |
| 3          | 14.8  | 70.5  | 21    | 10     | US-09-944-326-2    |    | Sequence 2, Appli   |
| c 4        | 14.8  | 70.5  | 311   | 9      | US-10-196-107A-35  |    | Sequence 35, Appli  |
| c 5        | 14.8  | 70.5  | 311   | 10     | US-09-374-671-35   |    | Sequence 35, Appli  |
| c 6        | 14.2  | 67.6  | 21    | 9      | US-10-006-856A-163 |    | Sequence 163, Appli |
| c 7        | 14.2  | 67.6  | 22    | 9      | US-10-006-818A-163 |    | Sequence 163, Appli |
| c 8        | 14.2  | 67.6  | 22    | 9      | US-10-015-3A-163   |    | Sequence 163, Appli |
| c 9        | 14.2  | 67.6  | 26    | 9      | US-10-006-856A-164 |    | Sequence 164, Appli |
| c 10       | 14.2  | 67.6  | 26    | 9      | US-10-006-818A-164 |    | Sequence 164, Appli |
| c 11       | 13.8  | 65.7  | 28    | 9      | US-09-864-364-3    |    | Sequence 164, Appli |
| c 12       | 13.8  | 65.7  | 37    | 9      | US-10-196-107A-54  |    | Sequence 54, Appli  |
| c 13       | 13.8  | 65.7  | 37    | 10     | US-09-374-671-54   |    | Sequence 54, Appli  |
| c 14       | 13.8  | 65.7  | 24    | 4      | US-09-939-709-3    |    | Sequence 3, Appli   |
| c 15       | 13.6  | 64.8  | 24    | 4      | US-09-939-709-3    |    | Sequence 3, Appli   |
| c 16       | 13.6  | 64.8  | 49    | 9      | US-09-805-353-19   |    | Sequence 19, Appli  |
| c 17       | 13.6  | 64.8  | 50    | 9      | US-09-992-598-312  |    | Sequence 312, Appli |
| c 18       | 13.6  | 64.8  | 50    | 9      | US-09-989-293A-312 |    | Sequence 312, Appli |
| c 19       | 13.6  | 64.8  | 50    | 9      | US-09-989-735-312  |    | Sequence 312, Appli |

## ALIGNMENTS

RESULT 1  
US-09-944-326-4

Sequence 4, Application US/09944326

General Information:

File Reference: UBC\_P-020-2

Current Application Number: US/09-944,326

Current Filing Date: 2001-08-30

Prior Application Number: 60/121,726

Prior Filing Date: 1999-02-26

Prior Application Number: 09/913,325

Number of Seq ID NOS: 14

Software: PatentIn Ver. 2.1

Seq ID No 4

Length: 21

Type: DNA

Organism: HUMAN

Feature:

Other Information: antisense TRPM-2 0DN

US-09-944-326-4

Query Match 100.0%; Score 21; DB 10; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0;

Qy 1 CAGCAGAGAGTCTCATCAT 21

Db 1 CAGCAGAGAGTCTCATCAT 21

RESULT 2  
US-09-944-326-1

Sequence 1, Application US/09944326

Patent No. US200128220A1

General Information:

Applicant: Gleave, Martin

APPLICANT: Rennie, Paul S.  
 APPLICANT: Miyake, Hideaki  
 APPLICANT: Neilson, Colleen  
 TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY  
 FILE REFERENCE: UBC\_P-020-2  
 CURRENT APPLICATION NUMBER: US/09/944,326  
 CURRENT FILING DATE: 2001-08-30  
 PRIORITY FILING DATE: 1999-02-26  
 PRIORITY APPLICATION NUMBER: 09/121,726  
 PRIORITY APPLICATION NUMBER: 09/913,325  
 PRIORITY FILING DATE: 2001-08-10  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1  
 LENGTH: 21  
 TYPE: DNA  
 ORGANISM: Murine  
 FEATURE:  
 OTHER INFORMATION: antisense TRPM-2 0DN  
 US-09-944-326-1

Query Match 70.5%; Score 14.8; DB 10; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 4.9e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCAGGAGAGTCCTCAT 18  
 Db 4 CAGCAGGAGAGTCCTCAT 21

RESULT 3  
 Patent No. US20020128220A1  
 Sequence 2, Application US/0944326  
 GENERAL INFORMATION:  
 APPLICANT: Gleave, Martin  
 APPLICANT: Rennie, Paul S.  
 APPLICANT: Miyake, Hideaki  
 APPLICANT: Neilson, Colleen  
 TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY  
 FILE REFERENCE: UBC\_P-020-2  
 CURRENT APPLICATION NUMBER: US/09/944,326  
 CURRENT FILING DATE: 2001-08-30  
 PRIORITY APPLICATION NUMBER: 09/121,726  
 PRIORITY FILING DATE: 1999-02-26  
 PRIORITY APPLICATION NUMBER: 09/913,325  
 PRIORITY FILING DATE: 2001-08-10  
 NUMBER OF SEQ ID NOS: 14  
 SEQ ID NO 2  
 LENGTH: 21  
 TYPE: DNA  
 ORGANISM: Murine  
 FEATURE:  
 OTHER INFORMATION: mismatch control  
 US-09-944-326-2

Query Match 70.5%; Score 14.8; DB 10; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 4.9e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCAGGAGAGTCCTCAT 18  
 Db 4 CAGCAGGAGAGTCCTCAT 21

RESULT 4  
 US-10-196-107A-35/C  
 Sequence 35, Application US/10196107A  
 Publication No. US2003004931A1  
 GENERAL INFORMATION:  
 APPLICANT: Konieczny, Andrzej  
 APPLICANT: Morgenstern, Jay P.  
 APPLICANT: Karczynski, Andrzej  
 APPLICANT: Brauer, Andrew W.  
 TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
 NUMBER OF SEQUENCES: 104  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston

Bizindaukas, Christine B.  
 Brauer, Andrew W.  
 TITLE OF INVENTION: Allergenic Protein and Peptides from Dog  
 Dander and Uses Therefor  
 NUMBER OF SEQUENCES: 109  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lahive & Cockfield, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/196,107A  
 FILING DATE: 16-Jul-2002  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 09/374,671  
 FILING DATE: 1999-AUG-16  
 APPLICATION NUMBER: US 08/491,861  
 FILING DATE: 1995-OCT-27  
 APPLICATION NUMBER: PCT/US93/12468  
 FILING DATE: 1993-DEC-30  
 APPLICATION NUMBER: US 08/156,549  
 FILING DATE: 1993-NOV-22  
 APPLICATION NUMBER: US 07/999,712  
 FILING DATE: 1992-DEC-31  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DiGiorgio, Jeanne M.  
 REGISTRATION NUMBER: 41,710  
 REFERENCE/DOCKET NUMBER: IMI-026C2CNCPADV  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 742-4214  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 31 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
 US-10-196-107A-35

Query Match 70.5%; Score 14.8; DB 9; Length 31;  
 Best Local Similarity 88.9%; Pred. No. 5.1e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGCAGGAGAGTCCTCATC 19  
 Db 24 AGGAGGGGCTCTCATC 7

RESULT 5  
 US-09-374-671-35/C  
 Sequence 35, Application US/09374671  
 Patent No. US200201296A1  
 GENERAL INFORMATION:  
 APPLICANT: Morgenstern, Jay P.  
 APPLICANT: Karczynski, Andrzej  
 APPLICANT: Bizindaukas, Christine B.  
 APPLICANT: Brauer, Andrew W.  
 TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
 NUMBER OF SEQUENCES: 104  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston

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STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,671
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/491,861
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandaravours, Any E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-374-671-35

Query Match 70.5%; Score 14.8; DB 10; Length 31;
Best Local Similarity 88.9%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AGCAGCAGAGAGCTTCATC 19
Db 24 AGGAGCAGGCTTCATC 7

RESULT 6
US-10-006-856A-163/c
Sequence 163, Application US/10006856A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillian, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2830PIC14
CURRENT APPLICATION NUMBER: US/10/006,856A
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 163
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-856A-163

Query Match 70.5%; Score 14.8; DB 10; Length 31;
Best Local Similarity 88.9%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AGCAGCAGAGAGCTTCATC 19
Db 24 AGGAGCAGGCTTCATC 7

RESULT 7
US-10-006-818A-163/c
Sequence 163, Application US/10006818A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillian, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2830PIC14
CURRENT APPLICATION NUMBER: US/10/006,818A
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 163
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-818A-163

Query Match 70.5%; Score 14.2; DB 9; Length 22;
Best Local Similarity 84.2%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CAGCACAGAGCTTCATC 19
Db 22 CAGAACAGGGCTTCATC 4

RESULT 8
US-10-015-393A-163/c
Sequence 163, Application US/10015393A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillian, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2830PIC14
CURRENT APPLICATION NUMBER: US/10/006,856A
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 163
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-856A-163

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RESULT 9  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2830PIC46  
 CURRENT APPLICATION NUMBER: US/10/015.393A  
 CURRENT FILING DATE: 2002-06-10  
 Prior Application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 477  
 SEQ ID NO 163  
 LENGTH: 22  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic oligonucleotide probe  
 US-10-015-393A-163

Query Match 67.6%; Score 14.2; DB 9; Length 22;  
 Best Local Similarity 84.2%; Pred. No. 9.4e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 SEQ ID NO 164  
 LENGTH: 22  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic oligonucleotide probe  
 US-10-006-856A-164

RESULT 9  
 Sequence 164, Application US/10006856A  
 Publication No. US20030044811A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillian, Kenneth J.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2830PIC14  
 CURRENT APPLICATION NUMBER: US/10/006.856A  
 CURRENT FILING DATE: 2002-05-10  
 NUMBER OF SEQ ID NOS: 477  
 Prior Application removed - See File Wrapper or Palm  
 SEQ ID NO 164  
 LENGTH: 26  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic oligonucleotide probe  
 US-10-006-856A-164

Query Match 67.6%; Score 14.2; DB 9; Length 26;  
 Best Local Similarity 84.2%; Pred. No. 9.6e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 SEQ ID NO 165  
 LENGTH: 26  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic oligonucleotide probe  
 US-10-015-393A-165

RESULT 10  
 Sequence 164, Application US/10006818A  
 Publication No. US20030054468A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David

APPLICATION NUMBER: US 07/999,712  
FILING DATE: 1992-DEC-31  
ATTORNEY/AGENT INFORMATION:  
NAME: DIGIorgio, Jeannine M.  
REGISTRATION NUMBER: 41,710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-4700  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 54:  
US-10-196-107A-54

Query Match 65.7%; Score 13.8; DB 9; Length 37;  
Best Local Similarity 88.2%; Pred. No. 1.6e-03; DB 9; Length 37;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 65.7%; Score 13.8; DB 9; Length 37;  
Best Local Similarity 88.2%; Pred. No. 1.6e-03; DB 9; Length 37;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 14  
US-09-374-671-54/c  
Sequence 54, Application US/09374671  
; Sequence No. US0020012983A1  
; GENERAL INFORMATION:  
; APPLICANT: Morgenstern, Jay P.  
; ATTORNEY: Kanleczky, Andrzej  
; REGISTRATION NUMBER: 104  
; TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragours, Amy E.  
; REGISTRATION NUMBER: 36,207  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 742-4214  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

RESULT 13  
US-10-196-107A-54/c  
Sequence 54, Application US/10196107A  
; Sequence No. US20030043691A1  
; GENERAL INFORMATION:  
; APPLICANT: Morgenstern, Jay P.  
; ATTORNEY: Konleczky, Andrzej  
; REGISTRATION NUMBER: 109  
; TITLE OF INVENTION: Allergenic Protein and Peptides from Dog  
; NUMBER OF SEQUENCES: 109  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lahive & Cockfield, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/196,107A  
; FILING DATE: 16-Jul-2002  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 09/374,671  
; FILING DATE: 1999-AUG-16  
; APPLICATION NUMBER: US 08/491,861  
; FILING DATE: 1995-OCT-27  
; APPLICATION NUMBER: PCT/US93/124468  
; FILING DATE: 1993-DEC-30  
; APPLICATION NUMBER: US 08/156,549  
; FILING DATE: 1993-NOV-22

Query Match 65.7%; Score 13.8; DB 9; Length 37;  
Best Local Similarity 88.2%; Pred. No. 1.6e-03; DB 9; Length 37;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 65.7%; Score 13.8; DB 9; Length 37;  
Best Local Similarity 88.2%; Pred. No. 1.6e-03; DB 9; Length 37;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 12  
US-09-864-364-3/c  
Sequence 3, Application US/09864364  
; Publication No. US2003005470A1  
; GENERAL INFORMATION:  
; APPLICANT: CHUGAISEIYAKU KABUSIKIGAISSA  
; TITLE OF INVENTION: No. US20030005470A1 - Human Animal Exhibiting Bone Metastasis of Tu  
; FILE REFERENCE: PH-1182US  
; CURRENT APPLICATION NUMBER: US/09/864,364  
; CURRENT FILING DATE: 2001-08-17  
; PRIORITY APPLICATION NUMBER: JP 2001-140538  
; PRIOR FILING DATE: 2001-05-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 3  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: IL-11 primer  
US-09-864-364-3

Query Match 65.7%; Score 13.8; DB 9; Length 28;  
Best Local Similarity 88.2%; Pred. No. 1.5e+03; DB 9; Length 28;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 65.7%; Score 13.8; DB 9; Length 28;  
Best Local Similarity 88.2%; Pred. No. 1.5e+03; DB 9; Length 28;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 12  
US-09-864-364-3/c  
Sequence 3, Application US/09864364  
; Publication No. US2003005470A1  
; GENERAL INFORMATION:  
; APPLICANT: CHUGAISEIYAKU KABUSIKIGAISSA  
; TITLE OF INVENTION: No. US20030005470A1 - Human Animal Exhibiting Bone Metastasis of Tu  
; FILE REFERENCE: PH-1182US  
; CURRENT APPLICATION NUMBER: US/09/864,364  
; CURRENT FILING DATE: 2001-08-17  
; PRIORITY APPLICATION NUMBER: JP 2001-140538  
; PRIOR FILING DATE: 2001-05-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 3  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: IL-11 primer  
US-09-864-364-3

Query Match 65.7%; Score 13.8; DB 9; Length 28;  
Best Local Similarity 88.2%; Pred. No. 1.5e+03; DB 9; Length 28;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 65.7%; Score 13.8; DB 9; Length 28;  
Best Local Similarity 88.2%; Pred. No. 1.5e+03; DB 9; Length 28;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-09-374-671-54

Query Match 65.7%; Score 13.8; DB 10; Length 37;  
 Best Local Similarity 88.2%; Pred. No. 1.6e+03; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 2;

Qy 2 AGCCAGCAGTCCTCAT 18  
 Db 30 AGGGCAGGTCCTCAT 14

RESULT 15

US-09-939-709-3

; Sequence 3, Application US/09939709

; Patent No. US2002007773A1

; GENERAL INFORMATION:

; APPLICANT: BARON, Roland E.

; APPLICANT: SIMS, Natalie

; APPLICANT: SABATAKOS, Georgios

; APPLICANT: NESTLER, Eric

; APPLICANT: CHEN, Jingshan

; APPLICANT: KELZ, Max

; TITLE OF INVENTION: Methods of Using Agents that Modulate Bone Formation and Inhibit

; TITLE OF INVENTION: Adipogenesis

; FILE REFERENCE: 044574-50045-US

; CURRENT APPLICATION NUMBER: US/09/939,709

; CURRENT FILING DATE: 2001-08-28

; PRIOR APPLICATION NUMBER: US 60/228,450

; PRIOR FILING DATE: 2000-06-29

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: Patentin version 3.1

; SEQ ID NO: 3

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide: SV40 primer

US-09-939-709-3

Query Match 64.8%; Score 13.6; DB 10; Length 24;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 4;

Qy 1 CAGCAGCAGTCCTCATCA 20  
 Db 3 CAGCAGTACCTCATCA 22

Search completed: April 18, 2003, 08:58:39  
 Job time : 108 secs

GenCore version 5.1.4-p5-4574  
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:44:37 ; Search time 1679 Seconds  
 (without alignments)  
 205.564 Million cell updates/sec

Title: PCT-US03-05305-4  
 Perfect score: 21  
 Sequence: 1 caggaggcaggatccatcat 21

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
 Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : EST :\*

1: em\_estba:\*

2: em\_estbum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estcov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hrc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hrc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estcom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pin:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_man:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

RESULT 1

AA916352

LOCUS

ohoe11\_s1

DEFINITION

similar to TR:Q1347

Q1347 RAGA. [1] ;

mRNA sequence.

AA916352.1

ACCESSION

AA916352

VERSION

1

KEYWORDS

EST.

ORGANISM

Homo sapiens

SOURCE

EuCarysta

Metazoa

Chordata

Craniata

Vertebrata

Euteleostomi

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Seq primer: -40m13 fwd. BT from Amersham  
 High quality sequence stop: 1.

FEATURES  
 Source  
 Location/Qualifiers  
 1. .46  
 /organism="Homo sapiens"  
 /db\_xref="TAXON:9606"  
 /clone="IMAGE:1473356"  
 /clone.lib="NCI\_GAP\_Co8"  
 /lab\_host="DBH10B"  
 /tissue\_type="adenocarcinoma"  
 /note="Organ: colon; Vector: PT773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
 ORIGIN  
 Query Match 70.5%; Score 14.8; DB 9; Length 46;  
 Best Local Similarity 88.9%; Pred. No. 7..3e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 /note="Lab host: DBH10B; Tissue type: adenocarcinoma; Vector: PT773D-Pac (Pharmacia); Organ: colon; Cloning method: ligated to Eco RI adaptors; Normalization: normalized; Library construction: Bento Soares and M. Fatima Bonaldo."

Query 1 CAGGAGCAGAGTCTCAT 18  
 ||||||| |||||||||  
 Db 20 CAGCAGCTTAGTCCTCAT 37

RESULT 2  
 W25663/C  
 LOCUS W25663 44 bp mRNA linear EST 25-NOV-1998  
 DEFINITION Soares\_fetal\_heart. NbHH198 Homo sapiens cDNA clone IMAGE:327110\_5, similar to gb:X15183\_cds1 HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); mRNA sequence.  
 ACCESSION W25663  
 VERSION W25663.1 GI:1303517  
 EST.  
 KEYWORDS human,  
 ORGANISM Homo sapiens  
 SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 44)  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lemton, G., Marr, M., Parsons, J., Riffkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
 Trace considered overall poor quality  
 Insert Length: 596 Std Error: 0.00  
 Seq primer: mob REGA-ET  
 High quality sequence stop: 1.

FEATURES  
 Source  
 Location/Qualifiers  
 1. .44  
 /organism="Homo sapiens"  
 /db\_xref="GDB:1261312"  
 /db\_xref="TAXON:9606"  
 /clone="Soares\_fetal\_heart\_nbHH198"  
 /clone.lib="Soares\_fetal\_heart\_nbHH198"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DBH10B (ampicillin resistant)"  
 /note="Organ: heart; Vector: PT773D (Pharmacia) with a

| BASE COUNT            |  | a                       | 8        | c            | 11        | g         | 12          | t           | 1    | others |
|-----------------------|--|-------------------------|----------|--------------|-----------|-----------|-------------|-------------|------|--------|
| <b>ORIGIN</b>         |  |                         |          |              |           |           |             |             |      |        |
| Query Match           | 69.5%  |                         | Score    | 14.6;        | DB        | 14;       | Length      | 44;         |      |        |
| Best Local Similarity | 81.0%  |                         | Pred.    | No.          | 8         | 8e+03;    |             |             |      |        |
| Matches               | 17;  | Conservative            | 0;       | Mismatches   | 4;        |           | Indels      | 0;          | Gaps | 0;     |
| QY                    | 1  | CAGCAGGAGAGCTTCATCAT 21 |          |              |           |           |             |             |      |        |
| Db                    | 26   | 1111 11 1111 1111       |          |              |           |           |             |             |      |        |
|                       |  | CAGCAGTAGGGTCATCAT 6    |          |              |           |           |             |             |      |        |
| <b>RESULT 3</b>       |  |                         |          |              |           |           |             |             |      |        |
| BH861678/C            | BH861678   | 50                      | bp       | DNA          |           |           | GSS         | 05-AUG-2002 |      |        |
| LOCUS                 | SALK_087727  | Arabidopsis             | thaliana | TDNA         | insertion | lines     | Arabidopsis |             |      |        |
| DEFINITION            | thaliana   | genomic                 | clone    | SALK_087727, | DNA       | sequence. |             |             |      |        |
| ACCESSION             | BH861678   |                         |          |              |           |           |             |             |      |        |
| VERSION               | BH861678.1   | GI:22097004             |          |              |           |           |             |             |      |        |
| KEYWORDS              | GSS.   |                         |          |              |           |           |             |             |      |        |
| SOURCE                | thale cress  |                         |          |              |           |           |             |             |      |        |
| ORGANISM              | Arabidopsis thaliana   |                         |          |              |           |           |             |             |      |        |
|                       | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;   |                         |          |              |           |           |             |             |      |        |
|                       | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;   |                         |          |              |           |           |             |             |      |        |
|                       | Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  |                         |          |              |           |           |             |             |      |        |
| REFERENCE             | 1 (bases 1 to 50)  |                         |          |              |           |           |             |             |      |        |
| AUTHORS               | Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R. |                         |          |              |           |           |             |             |      |        |
| TITLE                 | A Sequence-Indexed Library of Insertion Mutations in the   |                         |          |              |           |           |             |             |      |        |
| JOURNAL               | Arabidopsis Genome Unpublished (2001)  |                         |          |              |           |           |             |             |      |        |
| COMMENT               | Contact: Joseph R. Ecker   |                         |          |              |           |           |             |             |      |        |
|                       | Salk Institute Genomic Analysis Laboratory (SIGnAL)  |                         |          |              |           |           |             |             |      |        |
|                       | The Salk Institute for Biological Studies  |                         |          |              |           |           |             |             |      |        |
|                       | 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  |                         |          |              |           |           |             |             |      |        |
|                       | Tel: 858 453 4100 x1752  |                         |          |              |           |           |             |             |      |        |
|                       | Fax: 858 558 6379  |                         |          |              |           |           |             |             |      |        |
|                       | Email: ecker@salk.edu  |                         |          |              |           |           |             |             |      |        |
|                       | This is single pass sequence recovered from the left border of   |                         |          |              |           |           |             |             |      |        |
|                       | TDNA.  |                         |          |              |           |           |             |             |      |        |
|                       | Class: TDNA tagged.  |                         |          |              |           |           |             |             |      |        |
| FEATURES              | Location/Qualifiers  |                         |          |              |           |           |             |             |      |        |
| source                | /organism="Arabidopsis thaliana"   |                         |          |              |           |           |             |             |      |        |
|                       | /strain="Columbia"   |                         |          |              |           |           |             |             |      |        |
|                       | /db_xref="taxon:3702"  |                         |          |              |           |           |             |             |      |        |
|                       | /clone="SALK_087727"   |                         |          |              |           |           |             |             |      |        |
|                       | /clone_lib="Arabidopsis thaliana TDNA insertion lines"   |                         |          |              |           |           |             |             |      |        |
|                       | /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion   |                         |          |              |           |           |             |             |      |        |
|                       | elements. The resultant fragment for each line was   |                         |          |              |           |           |             |             |      |        |
|                       | directly sequenced to determine the genomic sequence at  |                         |          |              |           |           |             |             |      |        |
|                       | the site of insertion. Details of the protocols used can   |                         |          |              |           |           |             |             |      |        |
|                       | be found at <a href="http://signal.salk.edu/tdna_protocols.html">http://signal.salk.edu/tdna_protocols.html</a> "  |                         |          |              |           |           |             |             |      |        |
| BASE COUNT            | 10   | a                       | 14       | c            | 15        | g         | 11          | t           |      |        |
| ORIGIN                |  |                         |          |              |           |           |             |             |      |        |
| Query Match           | 66.7%  |                         | Score    | 14;          | DB        | 17;       | Length      | 50;         |      |        |
| Best Local Similarity | 100.0%   |                         | Pred.    | No.          | 1.7e+04;  |           |             |             |      |        |
| Matches               | 14;  | Conservative            | 0;       | Mismatches   | 0;        |           | Indels      | 0;          | Gaps | 0;     |

|                       |   |  |   |               |           |                 |                           |  |
|-----------------------|---|--|---|---------------|-----------|-----------------|---------------------------|--|
| QY                    | 3   | GCAGCAGAGTCCTTC 16   |   |               | QY        | 1               | CAGGAGCAGAGTCCTTCATCAT 21 |  |
| Db                    | 41  | GCAGCAGAGTCCTTC 28   |   |               | Db        | 1               | CAGCAGCAGCATACACATCAT 21  |  |
| RESULT                | 4   | A2802584   | A2802584  | 21 bp DNA     | linear    | GSS 16-FEB-2001 |                           |  |
| LOCUS                 | 2M0061105R  | Mouse 10kb plasmid UGC1M   | library   | Mus musculus  | genomic   |                 |                           |  |
| DEFINITION            | clone UGC2M006105 R   | DNA sequence.  |   |               |           |                 |                           |  |
| ACCESSION             | A2802584  |  |   |               |           |                 |                           |  |
| VERSION               | A2802584.1  | GI:129549407   |   |               |           |                 |                           |  |
| KEYWORDS              | GSS.  |  |   |               |           |                 |                           |  |
| SOURCE                | house mouse.  |  |   |               |           |                 |                           |  |
| ORGANISM              | Mus musculus  |  |   |               |           |                 |                           |  |
| REFERENCE             | 1 (bases 1 to 21)   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |   |               |           |                 |                           |  |
| AUTHORS               | Dunn D., Aoyagi A., Barber, M., Beaorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauern, A. and Wright, D., Weiss, R.  |  |   |               |           |                 |                           |  |
| TITLE                 | Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  |  |   |               |           |                 |                           |  |
| JOURNAL               | Unpublished (2000)  |  |   |               |           |                 |                           |  |
| COMMENT               | Contact: Robert B. Weiss  |  |   |               |           |                 |                           |  |
|                       | University of Utah Genome Center  |  |   |               |           |                 |                           |  |
|                       | University of Utah  |  |   |               |           |                 |                           |  |
|                       | Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  |  |   |               |           |                 |                           |  |
|                       | tel: 801 585 5606   |  |   |               |           |                 |                           |  |
|                       | Fax: 801 585 7177   |  |   |               |           |                 |                           |  |
|                       | Email: ddunn@genetics.utah.edu  |  |   |               |           |                 |                           |  |
|                       | Insert Length: 10000 Std Error: 0.00  |  |   |               |           |                 |                           |  |
|                       | Plate: 0061 row: I column: 05   |  |   |               |           |                 |                           |  |
|                       | Seq primer: CACACAGAAACACCTATGACC   |  |   |               |           |                 |                           |  |
|                       | Class: plasmid ends   |  |   |               |           |                 |                           |  |
|                       | High quality sequence stop: 21.   |  |   |               |           |                 |                           |  |
| FEATURES              | Location/Qualifiers   |  |   |               |           |                 |                           |  |
| Source                | 1. .21  |  |   |               |           |                 |                           |  |
|                       | Organism="Mus musculus"   |  |   |               |           |                 |                           |  |
|                       | /strain="C57BL/6J"  |  |   |               |           |                 |                           |  |
|                       | /db_xref="taxon:10090"  |  |   |               |           |                 |                           |  |
|                       | /clone="UUGC2M006105"   |  |   |               |           |                 |                           |  |
|                       | /clone_id="Mouse 10kb plasmid UGGC1M library"   |  |   |               |           |                 |                           |  |
|                       | /sex="Male"   |  |   |               |           |                 |                           |  |
|                       | /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-   |  |   |               |           |                 |                           |  |
|                       | /note="Vector: PWD42N; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  |  |   |               |           |                 |                           |  |
|                       | (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA Polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD2 (gi:14732141gb AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapter mouse DNA was annealed to adapter vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." |  |   |               |           |                 |                           |  |
| BASE COUNT            | 8 a   | 7 c  | 3 g   | 3 t           |           |                 |                           |  |
| ORIGIN                |   |  |   |               |           |                 |                           |  |
| Query Match           | 61.9%   | Score 13;  | DB 17;  | Length 21;    |           |                 |                           |  |
| Best Local Similarity | 76.2%   | Pred. No. 3e-04;   |   |               |           |                 |                           |  |
| Matches               | 16;   | Conservative   | 0;  | Mismatches 5; | Indels 0; | Gaps 0;         | Gaps 0;                   |  |
| RESULT                | 6   | AL649065   | AL649065  | mRNA          | linear    | EST 13-DEC-2001 |                           |  |
| LOCUS                 | AL649065  | AL649065   | xGC-gastrula Silurana tropicalis cDNA clone TGas034i01 5' |               |           |                 |                           |  |
| DEFINITION            |   |  | mRNA sequence.  |               |           |                 |                           |  |
| VERSION               | AL649065  | AL649065.1   | GI:17658059   |               |           |                 |                           |  |



|           |  |             |   |  |
|-----------|--|-------------|---|--|
| VERSION   | AU107928.1   | GI:13557450 | /db_xref="taxon: 9606"                                  |  |
| KEYWORDS  | human.   |             | /clone="GRV62402"                                       |  |
| SOURCE    | Homo sapiens   |             | /note="Sugano Homo sapiens cDNA library"                |  |
| ORGANISM  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |             | /note="Differential display comparison of untreated and |  |
| REFERENCE | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.             |             | dimethylfumarate treated U937 cells"                    |  |
| AUTHORS   | 1 (bases 1 to 50)  |             | BASE COUNT  |  |
| SOURCE    | Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hatta   |             | ORIGIN  |  |
| COMMENT   | H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki       |             | Query Match   |  |
| COMMENT   | ,Y., Naramura,Y., Suyama,A. and Sugano,S.                              |             | Score 12.8; DB 9; Length 50;                            |  |
| FEATURES  | Diverse transcriptional initiation revealed by fine, large-scale       |             | Best Local Similarity                                   |  |
| SOURCE    | mapping of mRNA start sites  |             | 87.5%; Pred. No. 5.9e+04;                               |  |
| COMMENT   | EMBO Rep. 2 (5), 388-393 (2001)  |             | Matches 14; Conservative                                |  |
| COMMENT   | 2 (1-2), 149-156 (1997).   |             | 0; Mismatches 2; Indels 0; Gaps 0;                      |  |
| COMMENT   | Contact: Yutaka Suzuki   |             | QY 2 AGCAGCAGACTCTCA 17                                 |  |
| COMMENT   | Department of Virology   |             | DB 29 AGCAGCAGACTCCGCA 44                               |  |
| COMMENT   | Institute of Medical Science, University of Tokyo                      |             | /db_xref="taxon: 9606"                                  |  |
| COMMENT   | 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan                   |             | /clone="GRV62402"                                       |  |
| COMMENT   | Email: ysuzuki@ims.u-tokyo.ac.jp                                       |             | /note="GRV62402"  |  |
| COMMENT   | Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. |             | /note="Differential display comparison of untreated and |  |
| COMMENT   | a 5'-end enriched cDNA library. Gene 200 (1-2), 149-156 (1997).        |             | dimethylfumarate treated U937 cells"                    |  |
| COMMENT   | Location/Qualifiers  |             | /note="GRV62402"  |  |
| COMMENT   | 1. 50  |             | /note="GRV62402"  |  |
| COMMENT   | /organism="Homo sapiens"   |             | /note="GRV62402"  |  |
| COMMENT   | /db_xref="taxon: 9606"   |             | /note="GRV62402"  |  |
| COMMENT   | /clone="GRV62402"  |             | /note="GRV62402"  |  |
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| COMMENT   | Location/Qualifiers  |             | /note="GRV62402"</                                      |  |

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| Query Match   | 60.0% | Score 12.6; DB 17;   | Length 39; | LOCUS  | AA561123  |
| Best Local Similarity   | 78.9% | Pred. No. 6.3e+04;   |            | DEFINITION   | v141c01_r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:97484 5' similar to TR:G9/2037 G972037 SUCCINATE       |
| Matches 15; Conservative 0; Mismatches 4;                         |       | Indels 0; Gaps 0;  |            | ACCESSION  | AA561123  |
|   |       |  |            | VERSION  | AA561123.1  |
|   |       |  |            | KEYWORDS   | DEHYDROGENASE ; mRNA sequence.  |
| Qy 2 AGCACAGATCTCTCATCA 20  |       |  |            | SOURCE   | EST   |
| Db 38 AGGGCAGATGTCTCCA 20   |       |  |            | ORGANISM   | Mus musculus  |
|   |       |  |            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Murinae; Mus. |   |
| RESULT 12   |       |  |            | REFERENCE 1 (bases 1 to 46)  |   |
| AI766391/c  |       | AI766391 43 bp mRNA linear EST 20-DEC-1999                         |            | AUTHORS  | Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,   |
| LOCUS   |       | whb1d04_x1 NCI-CGAP_Kid11 Homo sapiens cDNA clone IMAGE:385223 3'  |            | Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,    |   |
| DEFINITION  |       | similar to SW:COX2_HUMAN P0403 CYTOCHROME C OXIDASE POLYPEPTIDE II |            | Thelsing,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and  |   |
| ACCESSION   |       | ; mRNA sequence.   |            | Waterson,R.  |   |
| VERSION   |       | AI766391   |            | The Washu-HMMI Mouse EST Project   |   |
| EST.  |       | AI766391.1 GI:5232900  |            | Unpublished (1996)   |   |
| KEYWORDS  |       |  |            | Comment  | Contact: Maria M/Mouse EST Project  |
| SOURCE  |       |  |            |  | Washu-HMMI Mouse EST Project  |
| ORGANISM  |       |  |            |  | Washington University School of Medicine  |
| Homo sapiens  |       |  |            |  | 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108   |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |       |  |            |  | Tel. 314 286 1800   |
| Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.       |       |  |            |  | Fax. 314 286 1810   |
| 1 (bases 1 to 43)   |       |  |            |  | Email: mouseest@watson.wustl.edu  |
| REFERENCE   |       | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.                      |            |  | This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. |
| AUTHORS   |       | National Cancer Institute, Cancer Genome Anatomy Project (CGAP),   |            |  | MGI:555512  |
| TITLE   |       | Tumor Gene Index   |            |  | Trace considered overall poor quality   |
| JOURNAL   |       | Unpublished (1997)   |            |  | Possible reversed clone; similarity on wrong strand   |
| COMMENT   |       | Contact: Robert Strausberg, Ph.D.                                  |            |  | Seq primer: -28ml3 rev1 EST from Amersham   |
|   |       | Email: cgaps-r@mail.nih.gov  |            |  | High quality sequence shop: 1.  |
|   |       | Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  |            |  | 1. .46  |
|   |       | Emmert-Buck, M.D. Ph.D.  |            |  | /organism="Mus musculus"  |
|   |       | CDNA Library Preparation: M. Bento Soares, Ph.D.                   |            |  | /strain="C57BL/6"   |
|   |       | CDNA Library Arrayed by: Greg Lennon, Ph.D.                        |            |  | /db_xref="taxon:10090"  |
|   |       | DNA Sequencing by: Washington University Genome Sequencing Center  |            |  | /clone="IMAGE:374784"   |
|   |       | Clone distribution: NCI-CGAP clone distribution information can be |            |  | /clone_lib="Stratagene mouse skin (#937313)"  |
|   |       | found through the I.M.A.G.E. Consortium/LLNL at:                   |            |  | /sex="females"  |
|   |       | www-bio.llnl.gov/obrp/image/image.html                             |            |  | /tissue_type="whole skin"   |
|   |       |  |            |  | /dev_stag="11 weeks old"  |
|   |       | Trace considered overall poor quality                              |            |  | /lab_host="SOLR (kanamycin resistant)"  |
|   |       | Insert Length: 641 Std Error: 0.00                                 |            |  | /Site_1: EcoRI  |
|   |       | Seq primer: -40UP from Gibco                                       |            |  | /Site_2: XbaI; Cloned unidirectionally. Primer: Oligo   |
|   |       | High quality sequence stop: 1.                                     |            |  | dr. Whole skin from 11 week old C57BL/6 female mice.  |
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|   |       | 1..43  |            |  | adaptor sequence: 5' GAATTCGGACGAG 3'; adaptor  |
|   |       | /organism="Homo sapiens"   |            |  | sequence: 5' CCGAGTTTTTTTTTTTTT 3'."  |
|   |       | /db_xref="taxon:9606"  |            |  | 11 a 11 c 15 g 9 t  |
|   |       | /clone="IMAGE:2385223"   |            |  | BASE COUNT  |
|   |       | /clone_id="NCI-CGAP_Kid11"   |            |  | ORIGIN  |
|   |       | /lab_host="DH10B"  |            |  | Query Match 60.0%; Score 12.6; DB 9; Length 46;   |
|   |       | /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with          |            |  | Best Local Similarity 78.9%; Pred. No. 6.9e+04; Mismatches 4; Indels 0; Gaps 0;   |
|   |       | a modified polylinker; Site_1: Not I; Site_2: Eco RI;              |            |  | RESULTS 14  |
|   |       | Plasmid DNA from the normalized library NCI-CGAP_Kid3 was          |            |  | AU105963  |
|   |       | prepared, and ss circles were made in vitro. Following HAP         |            |  | LOCUS AU105963/C  |
|   |       | purification, this DNA was used as tracer in a subtractive         |            |  | DEFINITION AU105963 Sugano Homo sapiens cDNA library  |
|   |       | hybridization reaction. The driver was PCR-amplified cDNAs         |            |  | COLP3356, mRNA sequence.  |
|   |       | from a pool of 5,000 clones made from the same library             |            |  | ACCESSION AU105963  |
|   |       | (cloneIDs 1322376-1323911, 1456007-1456775, and                    |            |  | VERSION AU105963.1  |
|   |       | 1500552-1502855). Subtraction by Bento Soares and M.               |            |  | SOURCE EST.   |
|   |       | Fatima Bonaldo. "  |            |  | ORGANISM Homo sapiens   |
| BASE COUNT  | 10 a  | 5 c 21 g 7 t   |            |  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |
| ORIGIN  |       |  |            |  | AA561123/c  |
| Query Match   | 60.0% | Score 12.6; DB 9;  | Length 43; |  |   |
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| Matches 15; Conservative 0; Mismatches 4;                         |       | Indels 0; Gaps 0;  |            |  |   |
|   |       |  |            |  |   |
| Qy 1 CAGCACAGATCTCATC 19  |       |  |            |  |   |
| Db 32 CATCATCATCTCTCATC 14  |       |  |            |  |   |
|   |       |  |            |  |   |
| RESULT 13   |       |  |            |  |   |
|   |       |  |            |  |   |

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo. 1 (bases 1 to 50) Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki

Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano S., Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES Location/Qualifiers

Source

1. .50 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="COLF6356"  
 /clone.lib="Sugano Homo sapiens cDNA library"  
 /note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT

ORIGIN

Query Match 60.08; Score 12.6; DB 9; Length 50;  
 Best Local Similarity 78.98; Pred. No. 7.2e+04;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCCTCACCA 20

Db 11 a 14 c 13 g 12 t

RESULT 15

AU105967/c LOCUS AU105967 Sugano Homo sapiens 50 bp mRNA linear EST 30-AUG-2001 DEFINITION AU105967 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC05018, mRNA sequence.

ACCESSION AU105967

VERSION AU105967.1 GI:13555488

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki

Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan

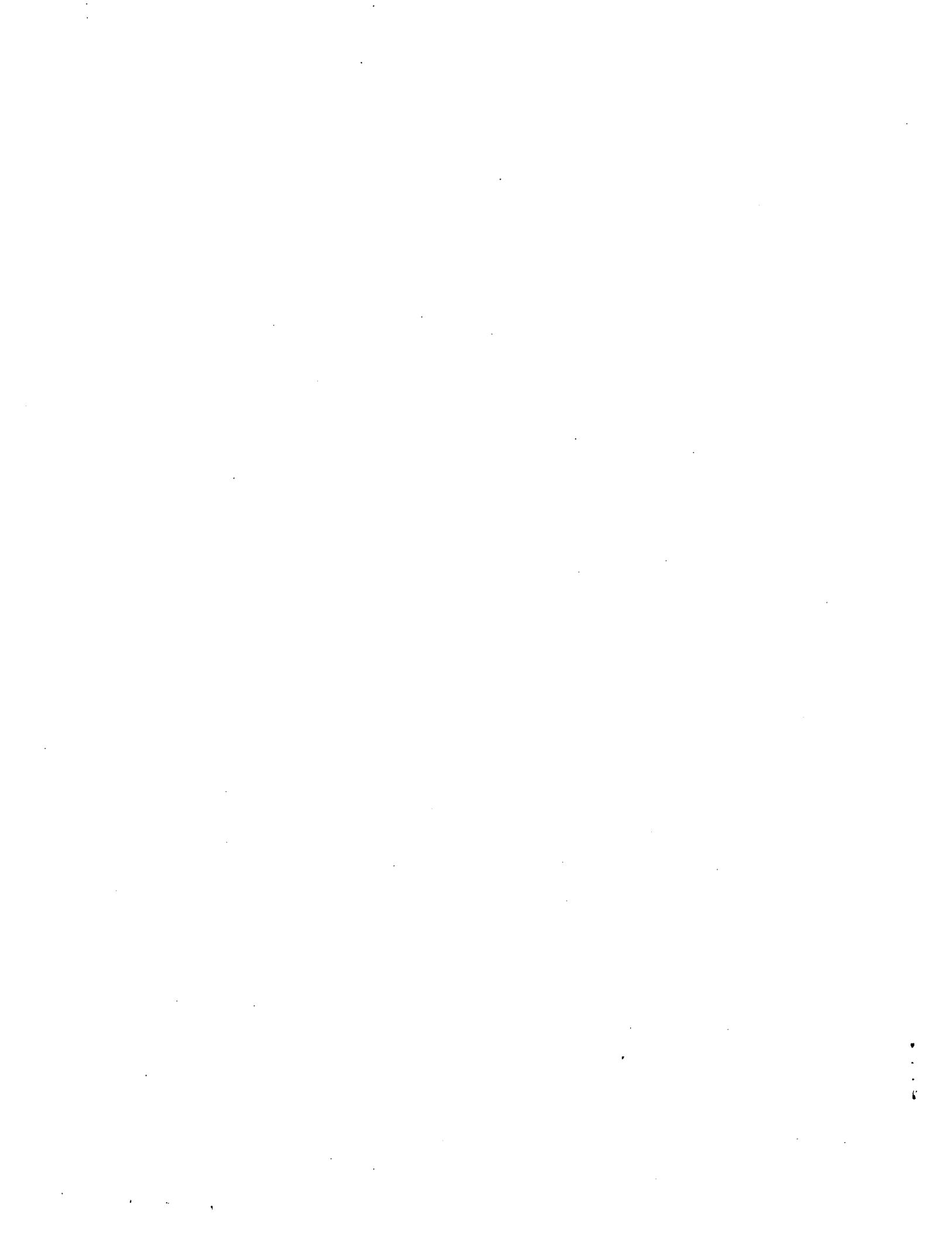
Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano S., Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES Location/Qualifiers

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1. .50 /organism="Homo sapiens"  
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 /note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"





**Claim 3:** Page 36; 38pp; English.

The present sequence is an antisense oligonucleotide directed at the human testosterone-repressed prostate message-2 (TRPM-2, also known as clusterin, sulfated glycoprotein-2 or SGP 2). The sequence was shown to promote the regression of tumours, and oligonucleotides directed at human TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2 gene. These include prostate cancer, renal cell cancer and some breast cancer cells. In addition to this, they also increase the chemosensitivity of the cells, meaning that conventional chemotherapy is more effective.

Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 other;

| Query Match           | Score  | DB         | Length |
|-----------------------|--------|------------|--------|
| Best Local Similarity | 100.0% | 21         | 21     |
| Matches               | 100.0% | Pred. No.  | 3.2;   |
| Matches               | 21;    | Mismatches | 0;     |
|                       |        | Indels     | 0;     |
|                       |        | Gaps       |        |

AX24790/C  
D AX24790 standard; DNA; 50 BP.

AX24790;

Y Y 1 CAGCAGCAGAGTCTTCATCAT 21  
X X 1 ||||| ||||| ||||| |||||  
b b 1 CAGCAGCAGAGTCTTCATCAT 21

**RESULT 2**  
AX24790/C  
D AX24790 standard; DNA; 50 BP.

AX24790;

Y Y 1 CAGCAGCAGAGTCTTCATCAT 21  
X X 1 ||||| ||||| ||||| |||||  
b b 1 CAGCAGCAGAGTCTTCATCAT 21

21-JUN-1999 (first entry)

Interleukin-18 binding protein splice variant IL-18BPA PCR primer.

Interleukin-18 binding protein; IL-18BPA; splice variant; human; autoimmune disease; inflammation; diabetes; Pancreatitis; rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis; psoriasis; inflammatory bowel disease; multiple sclerosis; ischemic heart disease; ischemic brain injury; gene therapy; PCR; primer; ss.

Synthetic.  
Homo sapiens.  
WO9909063-A1.

25-FEB-1999.

F F 13-AUG-1998; 98WO-IL00379.

R R 22-JUL-1998; 98IL-0125463.

R R 14-AUG-1997; 97IL-0121554.

R R 27-AUG-1997; 97IL-0121639.

R R 29-SEP-1997; 97IL-0121860.

R R 06-NOV-1997; 97IL-0122134.

(YEDA ) YEDA RES & DEV CO LTD.

Dinarello C, Kim SH, Novick D, Rubinstein M;

WPI; 1999-180975/15.

New interleukin-18 binding protein - useful for treating human diseases, including autoimmune disease and inflammation

Example 7: Page 39; 100pp; English.

The present sequence is a reverse primer that was used with a forward primer (see AX24754) in the PCR amplification of the coding region of a cDNA clone (see AX24749) coding for human interleukin-18 binding protein splice variant IL-18BPA (see AAW98004). The PCR products were cut with XbaI and cloned into the XbaI site of the pCOS7 BPA expression vector. IL-BPA18 was expressed in transfected COS7 cells. The invention provides IL-18BPA polynucleotides capable of

|  |
|--|
| binding IL-18 and/or modulating and/or blocking IL-18 activity.  |
| These can be used to treat conditions requiring the protein (claimed), such as autoimmune diseases, type I diabetes, rheumatoid arthritis, graft rejections, inflammatory bowel disease, sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain injury, chronic hepatitis, psoriasis, and chronic/acute pancreatitis. |
| XX Sequence 50 BP; 13 A; 8 C; 13 G; 16 T; 0 other;   |
| Query Match 84.8%; Score 17.8; DB 20; Length 50;   |
| Best Local Similarity 90.5%; Pred. No. 99; Gaps  |
| Matches 19; Conservative 0; Mismatches 2; Indels 0;  |
| XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps  |
| AAA09140 standard; DNA; 32 BP.   |
| AAA09140   |
| XX   |
| AC   |
| AAA09140;  |
| XX 10-AUG-2000 (first entry)   |
| DT XX DE Gos-2 promoter gene-specific primer 1.  |
| XX XX maize; promoter; actin-2; enolase; Gos-2; L41; gene expression;  |
| KW regulation; plant transformation; primer; ss.   |
| XX Zea mays  |
| OS XX PN WO2000020571-A2.  |
| XX PD 13-APR-2000.   |
| XX 05-OCT-1999; 9960-US23081.  |
| XX PF 05-OCT-1998; 9805-0103294.   |
| PR 05-NOV-1998; 9805-0107201.  |
| XX XXX (PIONEER HI-BRED INT INC.   |
| PA (AGER-) AGERI AGRIC GENETIC ENG RES INST.   |
| XX Barbour E, Meyer TE, Saad ME;   |
| XX WPI; 2000-303763/26.  |
| XX Novel maize promoters used for producing transgenic plants with   |
| PT regulated expression of heterologous nucleotide sequences   |
| PT Example 1; Page 26; 48pp; English.  |
| PS Novel maize promoters (AAA09134-37) that drive expression of actin-2,   |
| XX enolase, Gos-2 or L41, respectively, were isolated from genomic DNA   |
| CC using PCR. The first round of PCR was performed on each DNA sample  |
| CC using PCR. The first round of PCR was performed on each DNA sample wi   |
| CC Clontech primer API (AAA09138) and a gene-specific primer 1   |
| CC (AAA09139-42), in a second round of PCR using Clontech primer AP2   |
| CC (AAA09141) and gene-specific primer 2 (AAA09144-47). Clones were  |
| CC sequenced for verification and then amplified with Clontech primer AP   |
| CC (AAA09148) and a gene-specific primer (AAA09149-52). The promoters a  |
| CC used for regulating the expression of heterologous nucleotide sequences   |
| CC to vary the phenotype of a plant, e.g. modifying fatty acid composition   |
| CC altering amino acid content and altering the pathogen defense system  |
| CC the plant. Plants comprising important commercial traits can be   |
| CC generated.  |
| XX Sequence 32 BP; 8 A; 12 C; 6 G; 6 T; 0 other;   |
| Query Match 77.1%; Score 16.2; DB 21; Length 32;   |
| Best Local Similarity 85.7%; Pred. No. 4; 99+02;   |
| SQ   |



|   |   |   |  |
|---|---|---|--|
| KW  | pharmaceutical; BamHI; ss.  | PN  | WO200049937-A2.  |
| XX  |   | XX  | 31-AUG-2000.   |
| OS  | Synthetic.  | PD  |  |
| XX  |   | XX  | 25-FEB-2000; 2000WO-US04875.   |
| PN  | WO9963077-A2.   | PP  |  |
| XX  |   | XX  | 26-FEB-1999; 99US-0121726.   |
| PD  | 09-DEC-1999.  | PR  |  |
| XX  |   | XX  |  |
| PF  | 04-JUN-1999; 99NO-US12516.  | PA  | (UYBR-) UNIV BRITISH COLUMBIA.   |
| XX  |   | XX  |  |
| PR  | 04-JUN-1998; 98US-0087905.  | PI  | Gleave M, Rennie PS, Miyake H, Nelson C;   |
| PR  | 03-JUN-1999; 99US-0324672.  | XX  |  |
| XX  |   | DR  | WPI; 2000-533132/48.   |
| PA  | (TMNE-) TM TECHNOLOGIES INC.  | XX  |  |
| XX  |   | PT  | Treating prostatic tumors and renal cancers by antisense inhibition of the testosterone-repressed prostate messenger-2 gene -    |
| PI  | Lane MJ, Benight AS, Faldasz BD;  | PT  |  |
| XX  |   | XX  |  |
| DR  | WPI; 2000-116369/10.  | PS  | Example 1; Page 35; 38pp; English.   |
| XX  |   | XX  |  |
| PT  | Modulating polynucleotide ligand binding site affinity using PT determination of the flanking duplex sequences -  | XX  |  |
| XX  | Example 1; Page 45; 62pp; English.  | SQ  | Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 other;   |
| PS  |   | Query Match   | Score 14.8; DB 21; Length 21;  |
| XX  |   | Best Local Similarity                                       | 80.5%; Pred. No. 2e+03;  |
| CC  | The invention provides a method for determining the sequence of CC polynucleotides flanking regions that modulate ligand binding CC characteristics of an adjacent binding site. The method comprises:  | Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |  |
| CC  | (i) Providing a number of different duplex polynucleotides, each having CC the same polynucleotide ligand binding site and randomly synthesised CC sequence flanking the binding site; (ii) exposing the duplex to a ligand CC selective for the binding site; (iii) isolating duplexes which bind or CC do not bind the ligand; and (iv) determining the nucleotide composition CC of the flanking duplex sequence by sequencing the duplex sequence CC adjacent to the binding site. The invention is used to modulate the CC ligand-binding characteristics of any nucleotide sequence. The invention CC is less costly and more efficient than prior art techniques that moderate CC ligand binding using small molecule pharmaceuticals. Sequences CC AA25762-296170 represent polynucleotide sequences including the binding CC site for the restriction enzyme BamHI and used in the course of the CC invention. | Qy 1 CAGCAGGAGACTCTTCAAT 18                                 |  |
| CC  |   | Db 4 CAGCAGGAGACTCTTCAAT 21                                 |  |
| XX  | Sequence 40 BP; 6 A; 5 C; 19 G; 10 T; 0 other;  | RESULT 8  |  |
| SQ  |   | AAA94224  |  |
| Query Match   | 72.4%; Score 15.2; DB 21; Length 40;  | ID  | AAA94224 standard; DNA; 21 BP.   |
| Best Local Similarity   | 85.0%; Pred. No. 1.4e+03;   | XX  |  |
| Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;   | AC  | AAA94224;   |  |
| XX  |   | XX  | 12-JAN-2001 (first entry)  |
| Qy 1 CAGCAGGAGACTCTTCAAT 20   |   | DE  | Murine testosterone-repressed prostate message-2; TRPM-2; clusterin; KW  |
| Db 28 CAGCAACAGCTCTCCCTCA 9   |   | XX  | KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.  |
| XX  |   | XX  | RN sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.  |
| AC AAA94223;  |   | OS  | Nus sp.  |
| XX  |   | XX  | PN WO200049937-A2.   |
| AC AAA94223;  |   | PD  | 31-AUG-2000.   |
| XX  |   | XX  | 25-FEB-2000; 2000WO-US04875.   |
| DT 12-JAN-2001 (first entry)  |   | PP  |  |
| XX  |   | XX  | 26-FEB-1999; 99US-0121726.   |
| DE Murine testosterone-repressed prostate message-2 antisense oligo #1.   |   | PR  |  |
| XX  |   | XX  |  |
| KW Mouse; testosterone-repressed prostate message-2; TRPM-2; clusterin; KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss. |   | PA  | (UYBR-) UNIV BRITISH COLUMBIA.   |
| XX  |   | PI  | Gleave M, Rennie PS, Miyake H, Nelson C;   |
| OS Nus sp.  |   | XX  |  |
| XX  |   | DR  | WPI; 2000-533132/48.   |
| FH Key Location/Qualifiers  |   | XX  | Treating prostatic tumors and renal cancers by antisense inhibition of PT the testosterone-repressed prostate messenger-2 gene - |
| FT modified_base 1 /*tag= a /mod_base= OTHER  |   | XX  |  |
| FT FT /note= " phosphorothioate backbone"   |   | PS  | Example 1; Page 35; 38pp; English.   |
| XX  |   |   |  |





XX 28-JUN-2000; 2000CN-0116822.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie X;

PI DR; 2002-351761/38.

PT Homo transcription factor F19.02 and encoding polynucleotide, used in treatment of erythropathy

XX Example 4; Page 18; 38pp; Chinese.

XX The invention relates to an isolated polypeptide of human (Homo) transcription factor LCR-F19.02, the cDNA encoding it, and its fragment, analogue or derivative. Also included are vectors expressing the protein, a host cell comprising the vector, the isolation of modulators of the protein and an anti-transcription factor LCR-F19.02 antibody. The protein and nucleic acid are used in diagnosis and treatment of erythropathy. The present sequence is a PCR primer used to clone the cDNA encoding transcription factor LCR-F19.02.

SQ Sequence 33 BP; 7 A; 9 C; 8 G; 9 T; 0 other;

Query Match 69.5%; Score 14.6; DB 24; Length 33;

Best Local Similarity 0.1%; Pred. No. 2.6e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCAGCAGACTCTCATCAT 21

DB 27 CAACAGAAGGCCCTCATCAT 7

RESULT 15

AAX06964

ID AAX06964 standard; DNA; 44 BP.

XX AAX06964;

AC XX

DT 10-MAY-1999 (first entry)

XX Bacillus licheniformis xyloglucanase primer Xyloglu.upper.PstI.

DE XX

KW Xyloglucanase; detergent; PCR primer; ss.

XX Synthetic.

OS Bacillus licheniformis.

XX WO9902663-A1.

PN 21-JAN-1999.

XX PD 01-JUL-1998;

PF 98WO-DK00290.

XX PR 24-OCT-1997;

PR 97DK-0001213.

XX PR 07-JUL-1997;

PR 97DK-0000622.

XX PA (NOVO ) NOVO-NORDISK AS.

XX Bjornvad ME, Jorgensen PL, Outtrup H, Schuelein M;

PI DR; 1999-120866/10.

XX New enzyme preparation comprising a xyloglucanase with an activity of 50  $\mu$  at pH 7 - useful for improving the properties of cellulosic fibres, yarn, (non)woven fabric, and raffing hemp, jute, flax and linen fibres

PT PT

XX PA

XX Example 5; Page 60; 87pp; English.

PS DR;

XX PI; 1999-120866/10.

XX Primers Xyloglu.upper.PstI and Xyloglu.lower.NotI (see AAX06965) were used for the PCR amplification of *Bacillus licheniformis* ATCC 14580 xyloglucanase DNA (see also AAX05949), using chromosomal DNA as template. The primers incorporate PstI and NotI sites into the amplified DNA. The PCR product was ligated into plasmid pMOL944, a pB110 derivative containing elements making it propagatable in *Bacillus subtilis*. The *B. licheniformis* xyloglucanase (see AAB88462) was expressed in transformed *B. subtilis* PI2954 cells. The enzyme is useful for improving the properties of cellulosic fabrics and in detergent compositions.

XX SQ Sequence 44 BP; 7 A; 16 C; 12 G; 9 T; 0 other;

Query Match 69.5%; Score 14.6; DB 20;

Best Local Similarity 0.1%; Pred. No. 2.7e+03;

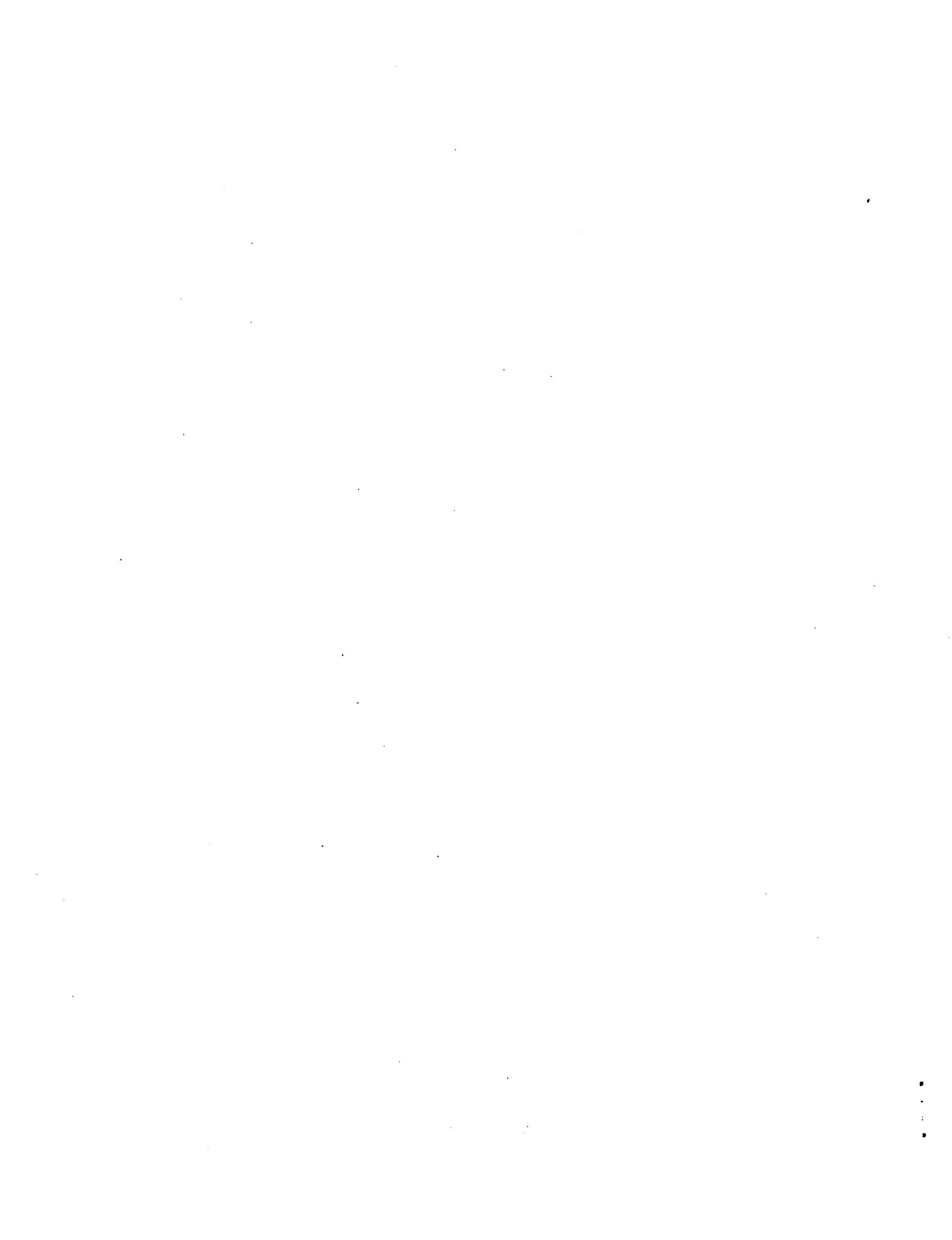
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCAGCAGACTCTCATCAT 21

DB 12 CAGCAGGCGGCGCTCTCAT 32

Search completed: April 18, 2003, 07:51:31

Job time : 239 secs



GenCore version 5.1.4\_P5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:47:42 ; Search time 52 Seconds  
(without alignments)  
123.850 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21

Sequence: 1. caggcaggatcttcatcat 21

Scoring table: IDENTITY\_NUC

GAPOP 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /cgn2\_6\_ptodata/1/ina/5A\_COMB.seq:  
2: /cgn2\_6\_ptodata/1/ina/5B\_COMB.seq:  
3: /cgn2\_6\_ptodata/1/ina/6A\_COMB.seq:  
4: /cgn2\_6\_ptodata/1/ina/6B\_COMB.seq:  
5: /cgn2\_6\_ptodata/1/ina/PCUTS\_COMBO.seq:  
6: /cgn2\_6\_ptodata/1/ina/backfile1.seq:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID              | Description         |
|------------|-------|-------|-------|--------|--------------------|---------------------|
| 1          | 15.4  | 73.3  | 45    | 1      | US-07-885-689A-7   | Sequence 7, Appli   |
| c 2        | 14.8  | 70.5  | 31    | 2      | US-08-467-603-35   | Sequence 35, Appli  |
| c 3        | 14.8  | 70.5  | 31    | 2      | US-08-466-793-35   | Sequence 35, Appli  |
| c 4        | 14.8  | 70.5  | 31    | 2      | US-08-491-861A-35  | Sequence 35, Appli  |
| c 5        | 14.6  | 69.5  | 44    | 4      | US-09-110-952A-11  | Sequence 11, Appli  |
| 6          | 14.2  | 67.6  | 20    | 2      | US-09-205-860-3    | Sequence 3, Appli   |
| 7          | 14.2  | 67.6  | 20    | 4      | US-09-657-452A-163 | Sequence 163, Appli |
| c 8        | 14.2  | 67.6  | 24    | 4      | US-09-360-545-57   | Sequence 57, Appli  |
| c 9        | 14.2  | 67.6  | 30    | 3      | US-09-130-663-10   | Sequence 10, Appli  |
| c 10       | 14.2  | 67.6  | 30    | 3      | US-09-432-335-10   | Sequence 10, Appli  |
| c 11       | 14.2  | 67.6  | 30    | 4      | US-09-254-022B-20  | Sequence 20, Appli  |
| c 12       | 14.2  | 67.6  | 30    | 4      | US-09-514-022-10   | Sequence 10, Appli  |
| c 13       | 13.8  | 65.7  | 18    | 2      | US-09-256-496-15   | Sequence 15, Appli  |
| c 14       | 13.8  | 65.7  | 37    | 2      | US-08-466-603-54   | Sequence 54, Appli  |
| c 15       | 13.8  | 65.7  | 37    | 2      | US-08-466-793-54   | Sequence 54, Appli  |
| c 16       | 13.8  | 65.7  | 37    | 2      | US-08-491-861A-54  | Sequence 54, Appli  |
| c 17       | 13.6  | 64.8  | 20    | 4      | US-09-517-467B-87  | Sequence 6, Appli   |
| c 18       | 13.6  | 64.8  | 23    | 4      | US-09-489-085A-6   | Sequence 6, Appli   |
| c 19       | 13.6  | 64.8  | 27    | 6      | 5463174-1          | Patent No. 5463174  |
| c 20       | 13.4  | 63.8  | 20    | 4      | US-09-657-552A-162 | Sequence 162, Appli |
| c 21       | 13.4  | 63.8  | 34    | 1      | US-08-373-12A2-27  | Sequence 27, Appli  |
| c 22       | 13.4  | 63.8  | 34    | 1      | US-08-435-628-27   | Sequence 27, Appli  |
| c 23       | 13.2  | 62.9  | 18    | 2      | US-09-205-860-28   | Sequence 28, Appli  |
| c 24       | 13.2  | 62.9  | 24    | 4      | US-09-442-099A-9   | Sequence 9, Appli   |
| c 25       | 13.2  | 62.9  | 33    | 2      | US-08-343-643-100  | Sequence 100, Appli |
| c 26       | 13.2  | 62.9  | 38    | 3      | US-09-130-663-26   | Sequence 26, Appli  |
| c 27       | 13.2  | 62.9  | 38    | 3      | US-09-432-335-26   | Sequence 26, Appli  |

ALIGNMENTS

RESULT 1  
US-07-885-689A-7  
; Sequence 7, Application US/07885689A  
; Patent No. 5366876  
; GENERAL INFORMATION:  
; APPLICANT: Cho, Joong M.  
; APPLICANT: Lee, Tae H.  
; APPLICANT: Chung, Hyun H.  
; APPLICANT: Lee, Yong B.  
; APPLICANT: Lee, Tae G.  
; APPLICANT: Park, Young W.  
; APPLICANT: Han, Kyu B.  
; TITLE OF INVENTION: Method for Production of Bovine Growth Hormone using a Synthetic Gene.  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolash & Birch  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC/MS-DOS  
; SOFTWARE: Patent Release #1., Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/885,689A  
; FILING DATE: 19-MAY-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svensson, Leonard R.  
; REGISTRATION NUMBER: 30,330  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-241-1300  
; TELEFAX: 703-241-2848  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..45  
; OTHER INFORMATION: /label= oligonucleotide

OTHER INFORMATION: /note= "U7 oligonucleotide portion of synthetic  
US-07-885-889A-7 BGH gene, Figure 1."

Query Match 73.3%; Score 15.4; DB 1; Length 45;  
Best Local Similarity 94.1%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCAGTCCTTCATCA 20  
Db 21 CAGCAGTCCTCACCA 37

RESULT 2 US-08-466-793-35/c  
Sequence 35, Application US/08467603  
Patent No. 5843672

GENERAL INFORMATION:  
APPLICANT: Morgenstern, Jay P.  
APPLICANT: Kanieczny, Andrzej  
APPLICANT: Bizindaukas, Christine B.  
APPLICANT: Brauer, Andrew W.  
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog Dander and Uses Therefor

NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,793  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-026CP(1PC-048CP)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-466-793-35

Query Match 70.5%; Score 14.8; DB 2; Length 31;  
Best Local Similarity 90.9%; Pred. No. 3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGCAGCAGAGCTCTCATC 19  
Db 24 AGGAGCAGGGCTCTCATC 7

RESULT 4 US-08-491-861A-35/c  
Sequence 35, Application US/08491861A  
Patent No. 593983

GENERAL INFORMATION:  
APPLICANT: Morgenstern, Jay P.  
APPLICANT: Kanieczny, Andrzej  
APPLICANT: Bizindaukas, Christine B.  
APPLICANT: Brauer, Andrew W.  
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog Dander and Uses Therefor

NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street

CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/491,861A  
FILING DATE: 27-OCT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/999,712  
FILING DATE: 31-DEC-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMM-026CP (IPC-048CP)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
S-08/491-861A-35

| Query   | Match | Best Local   | Similarity | Score | DB         | Length | 31;    |
|---------|-------|--------------|------------|-------|------------|--------|--------|
| Matches | 16:   | Conservative | 88.9%      | 0     | Mismatches | 2      | Indels |
|         |       |              |            | 0     | 0          | 0      | 0      |

2 AGCAGCAGGAGCTCTCATC 19  
1 AGGAGCAGGAGCTCTCATC 11  
24 AGGAGCAGGAGCTCTCATC 7

RESULT 5

Sequence 11, Application US/09110959A  
Patent No. 6268197  
GENERAL INFORMATION:

APPLICANT: Schneid, Martin  
APPLICANT: Outtrup, Helle  
APPLICANT: Jørgensen, Per Lima

TITLE OF INVENTION: Alkaline Xyloglucanase  
FILE REFERENCE: 5206.200-US

CURRENT FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 08222/97  
PCT/US FILING DATE: 1997-07-07

PRIOR APPLICATION NUMBER: 1213/97  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/054,039

PRIOR APPLICATION NUMBER: 60/063,694  
PRIOR FILING DATE: 1997-10-28

SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 11  
SEQUENCE:

TYPE: DNA ORGANISM: *Bacillus* sp.  
IS-09-110-959A-11

Best Local Similarity 81.0%;  
Matches 17; Conservative  
Query Match 0.94%;  
Score 14.0%; DB 4%; Length 44%;  
Pred. No. 3.8e+02; Indels 0; Gaps 0;

RESULT 7

US 057 426 103  
Sequence 163, Application US/09657452A  
; Patent No. 6426188  
; GENERAL INFORMATION:

APPLICANT: Jacqueline Wyatt  
TITLE OF INVENTION: ANTISENSE MODULATION COMPOUND  
FILED DECEMBER 6, 2001  
SERIAL NO. 09/725,255

CURRENT APPLICATION NUMBER: US/09/657,452A  
CURRENT FILING DATE: 2000-09-07  
NUMBER OF SEQ ID NOS: 178

SEQ\_ID\_NO 103  
LENGTH: 20  
TYPE: DNA

FEATURE: OTHER INFORMATION: Antisense Oligonucleotides

| Query | Match      | Score | 14.2        |
|-------|------------|-------|-------------|
| Best  | Local      | 67.68 | pred. No. 5 |
| Rest  | Similarity | 84.28 |             |

QY 1 CAGCAGCAGAGTCTCATC 19  
Matches 18; Conservative 0; Mismatches 0;

Db 2 CATCATCATAGTCTTCATC 20

RESULT 8  
US-09-360-545-57/c  
i. Sequence 57. Application US/09360545

PATENT NO. 6429014  
GENERAL INFORMATION:  
APPLICANT: Croteau, Rodney B  
APPLICANT: Bohlmann, Jorg

APPLICANT: Phillips, Michael A.  
TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

```

; FILE REFERENCE: wsur13885
; CURRENT APPLICATION NUMBER: US/09/360,545
; EARLIER FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052,249
; EARLIER FILING DATE: 1997-11-07
; CURRENT APPLICATION NUMBER: PCT/US98/14528
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide corresponding to amino acid
; OTHER INFORMATION: sequence set forth in SEQ ID NO:46
; FEATURE:
; NAME/KEY: misc_feature.
; LOCATION: 1..(24)
; OTHER INFORMATION: Oligonucleotide that corresponds to the conserved
; OTHER INFORMATION: amino acid sequence set forth in SEQ ID NO:46
; US-09-360-545-57

Query Match 67.6%; Score 14.2%; DB:4; Length 24;
Best Local Similarity 84.2%; Pred. No. 5.3e+02; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCCTCATC 19
DB 24 CAGCAGCAGGTCCTCCAAC 6

RESULT 9
US-09-130-663-10/C
; Sequence 10, Application US/09130663A
; Patent No. 6020163
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; TITLE OF INVENTION: LIPOCALIN HOMOLOG
; FILE REFERENCE: 97-24
; CURRENT APPLICATION NUMBER: US/09/130,663A
; CURRENT FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/054,867
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer: ZC13270
; US-09-130-663-10

Query Match 67.6%; Score 14.2%; DB:3; Length 30;
Best Local Similarity 84.2%; Pred. No. 5.5e+02; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCCTCATC 19
DB 27 CAGGAACAGGGCTTCATC 9

RESULT 10
US-09-132-335-10/C
; Sequence 10, Application US/09432335
; Patent No. 614370
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; TITLE OF INVENTION: LIPOCALIN HOMOLOG
; FILE REFERENCE: 97-24
; CURRENT APPLICATION NUMBER: US/09/432,335
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer: ZC13270
; US-09-132-335-10

Query Match 67.6%; Score 14.2%; DB:4; Length 30;
Best Local Similarity 84.2%; Pred. No. 5.5e+02; Gaps 0;

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RESULT 12  
 US-09-614-022-10/C  
 Sequence 10, Application US/09614022  
 Patent No. 6365716  
 GENERAL INFORMATION:  
 APPLICANT: Conklin, Darrell C.  
 TITLE OF INVENTION: LIPOCALIN HOMOLOG  
 FILE REFERENCE: 97-24  
 CURRENT APPLICATION NUMBER: US/09/614,022  
 CURRENT FILING DATE: 2000-07-11  
 PRIOR APPLICATION NUMBER: 09/130,663  
 PRIOR FILING DATE: 1998-08-06  
 PRIOR APPLICATION NUMBER: 60/054,867  
 PRIOR FILING DATE: 1997-08-06  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: PastSEQ for Windows Version 3.0  
 SEQ ID NO: 10  
 LENGTH: 30  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE: Other information: Oligonucleotide primer: zC13270  
 US-09-614-022-10

Query Match 67.6%; Score 14.2; DB 4; Length 30;  
 Best Local Similarity 84.2%; Pred. No. 5.5e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCCTCATC 19  
 Db 27 CAGGACAGGGTCTTATC 9

RESULT 13  
 US-09-556-496-15  
 Sequence 15, Application US/09256496  
 GENERAL INFORMATION:  
 APPLICANT: Lex M. Cowart  
 TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-12 EXPRESSION  
 FILE REFERENCE: RIS-0056  
 CURRENT APPLICATION NUMBER: US/09/256,496  
 CURRENT FILING DATE: 1999-02-23  
 NUMBER OF SEQ ID NOS: 86  
 SEQ ID NO: 15  
 LENGTH: 18  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-256-496-15

Query Match 65.7%; Score 13.8; DB 2; Length 18;  
 Best Local Similarity 88.2%; Pred. No. 7.8e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGACTCTTC 17  
 Db 1 CAGCAGCAGGACTCTCA 17

RESULT 14  
 US-08-467-603-54/C  
 Sequence 54, Application US/08466793  
 Patent No. 5845672  
 GENERAL INFORMATION:

APPLICANT: Morganstern, Jay P.  
 APPLICANT: Kaniecny, Andrzej P.  
 APPLICANT: Bizindaukas, Christine B.  
 TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog Dander and Uses Therefor  
 NUMBER OF SEQUENCES: 104  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 State Street, suite 510  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA

Query Match 65.7%; Score 13.8; DB 2; Length 37;  
 Best Local Similarity 88.2%; Pred. No. 8.5e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 AGCAGGAGACTCTCAT 18  
 Db 30 AGGAGGGTCTCAT 14

RESULT 15  
 US-08-466-793-54/C  
 Sequence 54, Application US/08466793  
 Patent No. 5891716  
 GENERAL INFORMATION:  
 APPLICANT: Morganstern, Jay P.  
 APPLICANT: Kaniecny, Andrzej P.  
 APPLICANT: Bizindaukas, Christine B.  
 TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog Dander and Uses Therefor  
 NUMBER OF SEQUENCES: 104  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 State Street, suite 510  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA

ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,793  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/156,549  
FILING DATE: 22-NOV-1993  
APPLICATION NUMBER: 07/999,712  
FILING DATE: 31-Dec-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

| Query   | Match | Best Local Similarity | Score      | DB 2     | Length |
|---------|-------|-----------------------|------------|----------|--------|
| Matches | 15;   | Conservative          | 65.78;     | 13.8;    | 37;    |
|         |       |                       | Pred. No.  | .83e+02; |        |
|         |       |                       | Mismatches | 2;       |        |
|         |       |                       | Indels     | 0;       |        |
|         |       |                       | Gaps       | 0;       |        |

search completed: April 18, 2003, 08:56:37  
Duration: 61 sec

GenCore version 5.1.4\_p5\_4578  
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## OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:05:10 ; Search time 1839 Seconds

(without alignments)  
332.332 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21  
Sequence: 1 cagcagcaggatcttcatcat 21

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Post-processing: Minimum Match 0\*

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_da:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_on:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pi:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_yi:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_sts:\*

27: em\_un:\*

28: em\_yi:\*

29: em\_htg\_hum:\*

30: em\_htg\_inv:\*

31: em\_htg\_other:\*

32: em\_htg\_mus:\*

33: em\_htg\_pln:\*

34: em\_htg\_rid:\*

35: em\_htg\_mam:\*

36: em\_htg\_vrt:\*

37: em\_sy:\*

38: em\_htg\_hum:\*

39: em\_htg\_mus:\*

40: em\_htg\_other:\*

41: em\_htg\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB · ID    | Description         |
|------------|-------|-------------|--------|------------|---------------------|
| c 1        | 16.2  | 77.1        | 48     | 6 A76301   | A76301 Sequence 7   |
| c 2        | 16.2  | 77.1        | 48     | 6 E01067   | E01067 DNA sequence |
| c 3        | 15.4  | 73.3        | 39     | 6 A08489   | A08489 B.taurus ge  |
| c 4        | 15.4  | 73.3        | 39     | 6 A12568   | A12568 fragment of  |
| c 5        | 15.4  | 73.3        | 45     | 6 A05116   | A05116 Oligonucleo  |
| c 6        | 15.2  | 72.4        | 22     | 6 AX26895  | AX26895 Sequence    |
| c 7        | 14.8  | 70.5        | 27     | 6 AX118356 | AX118356 Sequence   |
| c 8        | 14.8  | 70.5        | 31     | 6 A070079  | A070079 Sequence    |
| c 9        | 14.6  | 69.5        | 48     | 6 A76303   | A76303 Sequence     |
| c 10       | 14.4  | 68.6        | 39     | 6 A08490   | A08490 Oligonucleo  |
| c 11       | 14.4  | 68.6        | 39     | 6 A08491   | A08491 Oligonucleo  |
| c 12       | 14.4  | 68.6        | 39     | 6 A12569   | A12569 fragment of  |
| c 13       | 14.4  | 68.6        | 39     | 6 A12570   | A12570 fragment of  |
| c 14       | 14.2  | 67.6        | 20     | 6 A085567  | A085567 Sequence    |
| c 15       | 14.2  | 67.6        | 30     | 6 A70102   | A70102 Sequence     |
| c 16       | 14.2  | 67.6        | 30     | 6 A148235  | A148235 Sequence    |
| c 17       | 14.2  | 67.6        | 30     | 6 A204084  | A204084 Sequence    |
| c 18       | 13.8  | 65.7        | 18     | 6 A092800  | A092800 Sequence    |
| c 19       | 13.8  | 65.7        | 31     | 6 A36373   | A36373 Sequence     |
| c 20       | 13.8  | 65.7        | 37     | 6 A070094  | A070094 Sequence    |
| c 21       | 13.8  | 65.7        | 50     | 6 AX233374 | AX233374 Sequence   |
| c 22       | 13.6  | 64.8        | 50     | 6 AX080828 | AX080828 Sequence   |
| c 23       | 13.6  | 64.8        | 50     | 6 AY403425 | AY403425 Sequence   |
| c 24       | 13.4  | 63.8        | 34     | 6 A045234  | A045234 Sequence    |
| c 25       | 13.4  | 63.8        | 34     | 6 A52286   | A52286 Sequence     |
| c 26       | 13.2  | 62.9        | 18     | 6 A085592  | A085592 Sequence    |
| c 27       | 13.2  | 62.9        | 23     | 6 AX262444 | AX262444 Sequence   |
| c 28       | 13.2  | 62.9        | 26     | 6 AY462235 | AY462235 Sequence   |
| c 29       | 13.2  | 62.9        | 31     | 6 AY249499 | AY249499 Sequence   |
| c 30       | 13.2  | 62.9        | 32     | 6 AX339313 | AX339313 Sequence   |
| c 31       | 13.2  | 62.9        | 33     | 6 A36538   | A36538 Sequence     |
| c 32       | 13.2  | 62.9        | 33     | 6 A080171  | A080171 Sequence    |
| c 33       | 13.2  | 62.9        | 34     | 6 A93582   | A93582 Sequence     |
| c 34       | 13.2  | 62.9        | 34     | 6 BD012889 | BD012889 Nucleus 1  |
| c 35       | 13.2  | 62.9        | 34     | 6 BD00834  | BD00834 Nucleus 1   |
| c 36       | 13.2  | 62.9        | 35     | 6 AX225282 | AX225282 Sequence   |
| c 37       | 13.2  | 62.9        | 38     | 6 AR204099 | AR204099 Sequence   |
| c 38       | 13.2  | 62.9        | 47     | 6 AX114377 | AX114377 Sequence   |
| c 39       | 13.2  | 62.9        | 47     | 6 AX195012 | AX195012 Sequence   |
| c 40       | 13    | 61.9        | 23     | 6 A91622   | A91622 Sequence     |
| c 41       | 13    | 61.9        | 23     | 6 137350   | 137350 Sequence     |
| c 42       | 13    | 61.9        | 23     | 6 194200   | 194200 Sequence     |
| c 43       | 13    | 61.9        | 24     | 6 E29370   | E29370 Method for   |
| c 44       | 13    | 61.9        | 27     | 6 BD013233 | BD013233 DNA compr  |
| c 45       | 13    | 61.9        | 27     | 6 BD010314 | BD010314 DNA compr  |

## ALIGNMENTS

| RESULT 1 | LOCUS                  | DEFINITION | ACCESSION | VERSION | KEYWORDS | SOURCE | ORGANISM        | REFERENCE                           |
|----------|------------------------|------------|-----------|---------|----------|--------|-----------------|-------------------------------------|
| A76301   | Sequence 7 from Patent | W09319173. | A76301    | 48 bp   | DNA      | linear | PAT 19-OCT-1999 | AUGUSTIN, H.                        |
|          |                        |            | A76301    |         |          |        |                 | TITLE                               |
|          |                        |            |           |         |          |        |                 | JOURNAL                             |
|          |                        |            |           |         |          |        |                 | PATENT: WO 9319173-A 7 30-SEP-1993; |
|          |                        |            |           |         |          |        |                 | FORSSMANN, WOLFGANG (DE)            |

Pred. No. is the number of results predicted by chance to have a



ACCESSION A05116  
VERSION A05116.1 GI:345003  
KEYWORDS synthetic construct.  
ORGANISM synthetic construct  
FEATURES artificial sequences.  
SOURCE Location/Qualifiers  
1. .45  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
BASE COUNT 8 a 17 c 10 g 10 t  
ORIGIN

Query Match Score 15.4; DB 6; Length 45;  
Best Local Similarity 94.1%; Pred. No. 1.2e+04;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGCTTCATCA 20  
LOCUS AX268965 22 bp DNA linear PAT 29-OCT-2001  
DEFINITION Sequence 46 from Patent WO0175165.  
ACCESSION AX268965  
VERSION AX268965.1 GI:16541984  
KEYWORDS synthetic construct.  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1. .22  
AUTHORS Mcconlogue, L.C., Games, K.D., Yednock, T.A., Hua, T., Messersmith, E.  
TITLE Screening markers and methods for neurodegenerative disorders  
JOURNAL Patent; WO 0175165-A 46 11-OCT-2001;  
Elan Pharmaceuticals, Inc. (US)  
FEATURES Location/Qualifiers  
1. .22  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="forward primer 662>"  
BASE COUNT 6 a 8 c 3 g 5 t  
ORIGIN

Query Match Score 15.2; DB 6; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.6e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGAGCTTCATCA 20  
LOCUS AXL18356 27 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 3479 from Patent WO0129262.  
ACCESSION AXL18356  
VERSION AXL18356.1 GI:14035307  
KEYWORDS synthetic construct.  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1. (bases 1 to 27)  
AUTHORS Picoult-Newburg, L. and Pohl, M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent; WO 0129262-A 349 26-APR-2001;  
Orchid Biosciences, Inc. (US)  
FEATURES Location/Qualifiers  
1. .27  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Primer"  
1. .27  
/note="C3 linker"  
BASE COUNT 5 a 8 c 4 g 9 t  
ORIGIN

Query Match Score 14.8; DB 6; Length 27;  
Best Local Similarity 84.2%; Pred. No. 2.5e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCAGAGAGCTTCATCA 20  
LOCUS AR070079/C 31 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 35 from patent US 5891716.  
ACCESSION AR070079  
VERSION AR070079.1 GI:7220967  
KEYWORDS Unknown.  
ORGANISM Unclassified.  
REFERENCE 1. (bases 1 to 31)  
AUTHORS Morgenstern, J.P., Konieczny, A., Bizinkauskas, C.B. and Brauer, A.W.  
TITLE Allergenic Proteins and Peptides from dog dander and use therefor  
JOURNAL Patent; US 5891716-A 35 06-APR-1999;  
FEATURES Location/Qualifiers  
1. .31  
/organism="unknown"  
BASE COUNT 7 a 13 c 5 g 6 t  
ORIGIN

Query Match Score 14.8; DB 6; Length 31;  
Best Local Similarity 88.9%; Pred. No. 2.5e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGAGAGCTTCATCA 19  
LOCUS AR070079/C 31 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 35 from patent US 5891716.  
ACCESSION AR070079  
VERSION AR070079.1 GI:7220967  
KEYWORDS Unknown.  
ORGANISM Unclassified.  
REFERENCE 1. (bases 1 to 31)  
AUTHORS Morgenstern, J.P., Konieczny, A., Bizinkauskas, C.B. and Brauer, A.W.  
TITLE Allergenic Proteins and Peptides from dog dander and use therefor  
JOURNAL Patent; US 5891716-A 35 06-APR-1999;  
FEATURES Location/Qualifiers  
1. .31  
/organism="unknown"  
BASE COUNT 7 a 13 c 5 g 6 t  
ORIGIN

Query Match Score 14.8; DB 6; Length 31;  
Best Local Similarity 88.9%; Pred. No. 2.5e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGGAGAGAGCTTCATCA 19  
LOCUS A76303/C 48 bp DNA linear PAT 19-OCT-1999  
DEFINITION Sequence 9 from Patent WO9319173.  
ACCESSION A76303  
VERSION A76303.1 GI:6088390  
KEYWORDS unidentified.  
ORGANISM unidentified.  
REFERENCE 1. (bases 1 to 48)  
AUTHORS Maegert, H.  
TITLE DNA CODING FOR APHRODISIN  
JOURNAL Patent; WO 9319173-A 9 30-SEP-1993;  
FEATURES Location/Qualifiers  
1. .48  
/organism="unidentified"  
/db\_xref="taxon:32630"  
1. .48  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAB58601.1"  
/db\_xref="GI:6088391"  
/translation="MYKILVIALYESLAHA"  
BASE COUNT 7 a 14 g 19 t  
ORIGIN

Query Match 69.5%; Score 14.6; DB 6; Length 48;  
 Best Local Similarity 81.0%; Pred. No. 3e+04;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Version 04-JAN-1994

Qy 1 CAGCAGCAGAGTCCTCATAT 21  
 Db 21 CAGCAGCAGAGTCCTTACCAT 1

RESULT 10  
 A08490 A08490 39 bp DNA linear PAT 22-JUL-1993  
 DEFINITION Oligonucleotide 3.  
 ACCESSION A08490  
 VERSION 1 GI:413472  
 KEYWORDS synthetic construct.  
 ORGANISM synthetic construct.  
 artificial sequences.  
 1 (bases 1 to 39)  
 REFERENCES Harbour, G. C., Hoogerheide, J. G. and Garlick, R. L.  
 TITLE Enhanced bioactivity of mammalian somatotropin through selective  
 deamidation  
 JOURNAL Patent: EP 0263206-A 6 13-APR-1988;  
 THE UPJOHN COMPANY  
 FEATURES  
 source Location/Qualifiers  
 1. .39  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 BASE COUNT 7 a 12 c 10 g 10 t  
 ORIGIN

Query Match 68.6%; Score 14.4; DB 6; Length 39;  
 Best Local Similarity 93.8%; Pred. No. 3.8e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Version 04-JAN-1993

Qy 4 CAGCAGCAGTCCTCATC 19  
 Db 12 CAGCAGCAGTCCTTCACC 27

RESULT 11  
 A08491 A08491 39 bp DNA linear PAT 22-JUL-1993  
 DEFINITION Oligonucleotide 4.  
 ACCESSION A08491  
 VERSION 1 GI:413473  
 KEYWORDS synthetic construct.  
 synthetic construct.  
 artificial sequences.  
 1 (bases 1 to 39)  
 REFERENCES Harbour, G. C., Hoogerheide, J. G. and Garlick, R. L.  
 TITLE Enhanced bioactivity of mammalian somatotropin through selective  
 deamidation  
 JOURNAL Patent: EP 0263206-A 7 13-APR-1988;  
 THE UPJOHN COMPANY  
 FEATURES  
 source Location/Qualifiers  
 1. .39  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 BASE COUNT 8 a 11 c 10 g 10 t  
 ORIGIN

Query Match 68.6%; Score 14.4; DB 6; Length 39;  
 Best Local Similarity 93.8%; Pred. No. 3.8e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Version 04-JAN-1993

Qy 4 CAGCAGCAGTCCTCATC 19  
 Db 12 CAGCAGCAGTCCTTCACC 27

RESULT 12  
 A12569 A12569 39 bp DNA linear PAT 04-JAN-1994  
 DEFINITION fragment of synthetic somatotropin.  
 ACCESSION A12569  
 VERSION A12569.1 GI:491409  
 KEYWORDS synthetic construct.  
 ORGANISM synthetic construct.  
 artificial sequences.  
 Location/Qualifiers  
 1. .39  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 BASE COUNT 7 a 12 c 10 g 10 t  
 ORIGIN

Query Match 68.6%; Score 14.4; DB 6; Length 39;  
 Best Local Similarity 93.8%; Pred. No. 3.8e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Version 04-JAN-1994

Qy 4 CAGCAGCAGTCCTCATC 19  
 Db 12 CAGCAGCAGTCCTTCACC 27

RESULT 13  
 A12570 A12570 39 bp DNA linear PAT 04-JAN-1994  
 DEFINITION fragment of synthetic somatotropin.  
 ACCESSION A12570  
 VERSION A12570.1 GI:491410  
 KEYWORDS synthetic construct.  
 ORGANISM synthetic construct.  
 artificial sequences.  
 Location/Qualifiers  
 1. .39  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 BASE COUNT 8 a 11 c 10 g 10 t  
 ORIGIN

Query Match 68.6%; Score 14.4; DB 6; Length 39;  
 Best Local Similarity 93.8%; Pred. No. 3.8e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Version 04-JAN-1994

Qy 4 CAGCAGCAGTCCTCATC 19  
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RESULT 14  
 AR085567 AR085567 20 bp DNA linear PAT 01-SEP-2000  
 DEFINITION Sequence 3 from patent US 5981732.  
 ACCESSION AR085567  
 VERSION AR085567.1 GI:10012334  
 KEYWORDS Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 bases 1 to 20  
 AUTHORS Cowert, L. M.  
 JOURNAL Antisense modulation of G-alpha-13 expression  
 Patent: US 5981732-A 3 09-NOV-1999;  
 FEATURES Location/Qualifiers  
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 BASE COUNT 5 a 8 c 4 g 3 t  
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A70102 A70102 30 bp DNA linear PAT 07-MAY-1999

LOCUS Sequence 20 from Patent WO9810095.

DEFINITION A70102 GI:4774533

ACCESSION A70102.1

VERSION

KEYWORDS unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 30)

AUTHORS Thompson,A.H. and Schmidt,G.

TITLE CHARACTERISING DNA

JOURNAL Patent: WO 9810095-A-20 12-MAR-1998;

BRAX GENOMICS LTD (GB)

FEATURES Location/Qualifiers

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FEATURES Source

1..30

/organism="unidentified"

BASE COUNT /db\_xref="taxon:32644"

ORIGIN 5 a 10 c 8 g 7 t

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Best Local Similarity 84.28; Pred. No. 4.9e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCAGCACAGTCATC 21  
 Db 1 GCAGCACAGTCATC 19

Search completed: April 18, 2003, 08:26:54  
 Job time : 1855 secs

